SeqServer®
biology in silico

BLAST2 Search Results

Sequences	Help

Retrieval	BLAST2	FASTA	ClustalW	GCG Assembly	Phrap	Translation

BLAST2 Manual

Confidential -- Property of Incyte Genomics, Inc.   SeqServer Version 4.6 March 2001

Program: blastp
Sequence ID(s):

☐ PF-0459US_SEQIDNO:25/102 vs. genpept122

NCBI-BLASTP 2.0.10 [Aug-26-1999]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

Query= PF-0459US_SEQIDNO:25/102
        (150 letters)

Database: genpept122
        698,042 sequences; 216,183,515 total letters

Searching...done

Sequences producing significant alignments:	Score (bits)	E Value
☑ g2388627 chemokine [Homo sapiens]	307	7e-83
☑ g5881909 thymus-expressed chemokine [Mus musculus]	127	7e-29
☑ g2388629 chemokine [Mus musculus]	125	2e-28
☑ g6561400 CC chemokine 6Ckine-leu [Mus musculus]	48	6e-05
☑ g12025212 small inducible cytokine A21c [Mus musculus]	48	6e-05
☑ g12025210 small inducible cytokine A21b [Mus musculus]	48	6e-05
☑ g3169697 beta chemokine Exodus-2 [Mus musculus]	48	8e-05
☑ g6561402 CC chemokine 6Ckine-ser [Mus musculus]	46	3e-04
☑ g3947924 TCA4 [Mus musculus]	46	3e-04
☑ g2624927 beta chemokine [Mus musculus]	46	3e-04
☑ g2209189 TCA4 [Mus musculus]	46	3e-04
☑ g12025208 small inducible cytokine A21a [Mus musculus]	46	3e-04
☑ g6456876 thymic stroma chemokine-1 precursor [Homo sapiens]	46	3e-04
☑ g5921131 chemokine eotaxin3 [Homo sapiens]	45	4e-04
☑ g5669887 CC chemokine IMAC [Homo sapiens]	45	4e-04
☑ g4539796 small inducible cytokine subfamily A member 26 [Homo	45	4e-04
☑ g4263736 similar to cytokines; similar to A31767 (PID:g88665)	45	4e-04

☑	g4128129	secondary lymphoid tissue chemokine [Homo sapiens]	43	0.003
☑	g2624925	beta chemokine [Homo sapiens]	43	0.003
☑	g2335035	SLC [Homo sapiens]	43	0.003

Database: genpept122
  Posted date: Mar 1, 2001 9:38 AM
Number of letters in database: 216,183,515
Number of sequences in database: 698,042

Lambda   K   H
    0.322   0.133   0.419

Gapped
Lambda   K   H
    0.270   0.0470   0.230

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 62235040
Number of Sequences: 698042
Number of extensions: 2321593
Number of successful extensions: 6166
Number of sequences better than 10.0: 163
Number of HSP's better than 10.0 without gapping: 32
Number of HSP's successfully gapped in prelim test: 131
Number of HSP's that attempted gapping in prelim test: 6120
Number of HSP's gapped (non-prelim): 164
length of query: 150
length of database: 216,183,515
effective HSP length: 51
effective length of query: 99
effective length of database: 180,583,373
effective search space: 17877753927
effective search space used: 17877753927
T: 11
A: 40
X1: 16 (7.4 bits)
X2: 38 (14.8 bits)
X3: 64 (24.9 bits)
S1: 41 (22.0 bits)

Submit sequences to: [BLAST2 ▼] [Submit] [Reset]

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[Sequences]   [Help]

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        (150 letters)

Database: genpept122
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Searching...done

```
                                                              Score      E
Sequences producing significant alignments:                  (bits)   Value

☑ g2388627   chemokine [Homo sapiens]
                                                               307     7e-83
☑ g5881909   thymus-expressed chemokine [Mus musculus]
                                                               127     7e-29
☑ g2388629   chemokine [Mus musculus]
                                                               125     2e-28
```

>g2388627 chemokine [Homo sapiens]
        Length = 150

 Score = 307 bits (777), Expect = 7e-83
 Identities = 147/150 (98%), Positives = 147/150 (98%)

```
Query: 1   MNLWLLACLVAGFLGAWAPAVHAQGVFEDCCLAYHYPIGWAVLRRAWTYRIQEVSGSCNL 60
           MNLWLLACLVAGFLGAWAPAVH QGVFEDCCLAYHYPIGWAVLRRAWTYRIQEVSGSCNL
Sbjct: 1   MNLWLLACLVAGFLGAWAPAVHTQGVFEDCCLAYHYPIGWAVLRRAWTYRIQEVSGSCNL 60

Query: 61  PAAIFYLPKRHRKVCGNPKSREVQRAMKLLDARNKVFAKLRHNTQTFQAGPHAVKKLSSG 120
           PAAIFYLPKRHRKVCGNPKSREVQRAMKLLDARNKVFAKL HN QTFQAGPHAVKKLSSG
Sbjct: 61  PAAIFYLPKRHRKVCGNPKSREVQRAMKLLDARNKVFAKLHHNMQTFQAGPHAVKKLSSG 120

Query: 121 NSKLSSSKFSNPISSSKRNVSLLISANSGL 150
           NSKLSSSKFSNPISSSKRNVSLLISANSGL
Sbjct: 121 NSKLSSSKFSNPISSSKRNVSLLISANSGL 150
```

>g5881909 thymus-expressed chemokine [Mus musculus]
             Length = 144

 Score = 127 bits (316), Expect = 7e-29
 Identities = 71/143 (49%), Positives = 87/143 (60%), Gaps = 14/143 (9%)

```
Query: 1    MNLWLLACLVAGFLGAWAPAVHAQGVFEDCCLAYHYPIGWAVLRRAWTYRIQEVSGSCNL 60
            M LWL ACLVA F+GAW P VHAQG FEDCCL Y + I W VLR A   Y  QEVSGSCNL
Sbjct: 1    MKLWLFACLVACFVGAWMPVVHAQGAFEDCCLGYQHRIKWNVLRHARNYHQQEVSGSCNL 60

Query: 61   PAAIFYLPKRHRKVCGNPKSREVQRAMKLLDARNK-VFAKLRHNTQTFQAGPHAVKKLSS 119
             A  FY   R + VCGNP+    V+RAM++L AR + V K    ++QT +   + +K
Sbjct: 61   RAVRFYF--RQKVVCGNPEDMNVKRAMRILTARKRLVHWKSASDSQTERKKSNHMK---- 114

Query: 120  GNSKLSSSKFSNPISSSKRNVSL 142
                    SK  NP S+S R+ +L
Sbjct: 115  -------SKVENPNSTSVRSATL 130
```


>g2388629 chemokine [Mus musculus]
             Length = 144

 Score = 125 bits (312), Expect = 2e-28
 Identities = 70/143 (48%), Positives = 87/143 (59%), Gaps = 14/143 (9%)

```
Query: 1    MNLWLLACLVAGFLGAWAPAVHAQGVFEDCCLAYHYPIGWAVLRRAWTYRIQEVSGSCNL 60
            M LWL ACLVA F+GAW P VHAQG FEDCCL Y + I W VLR A   Y  QEVSGSCNL
Sbjct: 1    MKLWLFACLVACFVGAWMPVVHAQGAFEDCCLGYQHRIKWNVLRHARNYHQQEVSGSCNL 60

Query: 61   PAAIFYLPKRHRKVCGNPKSREVQRAMKLLDARNK-VFAKLRHNTQTFQAGPHAVKKLSS 119
             A  FY   R + VCGNP+     V+RA+++L AR + V K    ++QT +   + +K
Sbjct: 61   RAVRFYF--RQKVVCGNPEDMNVKRAIRILTARKRLVHWKSASDSQTERKKSNHMK---- 114

Query: 120  GNSKLSSSKFSNPISSSKRNVSL 142
                    SK  NP S+S R+ +L
Sbjct: 115  -------SKVENPNSTSVRSATL 130
```


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     Posted date: Mar 1, 2001 9:38 AM
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   Number of sequences in database: 698,042

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Graphical Viewer...

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